Figure 1

MAMSSGGSGGGVPEQEDSVLFRRGTGQSDDSDIWDDTALIKAYDKAVASFKHALKNG
DICETSGKPKTTPKRKPAKKNKSQKKNTAASLQQWKVGDKCSAIWSEDGCIYPATIA
SIDFKRETCVVVYTGYGNREEQNLSDLLSPICEVANNIEQNAQENENESQVSTDESE
NSRSPGNKSDNIKPKSAPWNSFLPPPPPMPGPRLGPGKPGLKFNGPPPPPPPPPPHL
LSCWLPPFPSGPPIIPPPPPICPDSLDDADALGSMLISWYMSGYHTGYYMGFRQNQK
EGRCSHSLN

Figure 2A

CGGGGCCCCACGCTGCGCACCCGCGGGTTTGCTATGGCGATGAGCAGCGGCGGCAGT
GGTGGCGGCGTCCCGGAGCAGGAGGATTCCGTGCTGTTCCGGCGCGGCACAGGCCAG
AGCGATGATTCTGACATTTGGGATGATACAGCACTGATAAAAGCATATGATAAAGCT
GTGGCTTCATTTAAGCATGCTCTAAAGAATGGTGACATTTGTGAAACTTCGGGTAAA
CCAAAAACCACACCTAAAAGAAAACCTGCTAAGAAGAATAAAAGCCAAAAGAAGAAT
ACTGCAGCTTCCTTACAACAGTGGAAAGTTGGGGACAAATGTTCTGCCATTTGGTCA
GAAGACGGTTGCATTTACCCAGCTACCATTGCTTCAATTGATTTTAAGAGAGAAACC
TGTGTTGTGGTTTACACTGGATATGGAAATAGAGAGGAGCAAAATCTGTCCGATCTA
CTTTCCCCAATCTGTGAAGTAGCTAATAATATAGAACAGAATGCTCAAGAGAATGAA
AATGAAAGCCAAGTTTCAACAGATGAAAGTGAGAACTCCAGGTCTCCTGGAAATAAA
TCAGATAACATCAAGCCCAAATCTGCTCCATGGAACCCCTTTCTCCCTCCACCACCC
CCCATGCCAGGGCCAAGACTGGGACCAGGAAAGCCAGGTCTAAAATTCAATGGCCCA
CCACCGCCACCGCCACCACCACCACCCCACTTACTATCATGCTGGCTGCCTCCATTT
CCTTCTGGACCACCAATAATTCCCCCACCACCTCCCATATGTCCAGATTCTCTTGAT
GATGCTGATGCTTTGGGAAGTATGTTAATTTCATGGTACATGAGTGGCTATCATACT
GGCTATTATATGGGTTTTAGACAAAATCAAAAAGAAGGAAGGTGCTCACATTCCTTA
AATTAAGGAGAAATGCTGGCATAGAGCAGCACTAAATGACACCACTAAAGAAACGAT
CAGACAGATCTGGAATGTGAAGCGTTATAGAAGATAACTGGCCTCATTTCTTCAAAA
TATCAAGTGTTGGGAAAGAAAAAAGGAAGTGGAATGGGTAACTCTTCTTGATTAAAA
GTTATGTAATAACCAAATGCAATGTGAAATATTTTACTGGACTCTTTTGAAAAACCA
TCTGTAAAAGACTGAGGTGGGGGTGGGAGGCCAGCACGGTGGTGAGGCAGTTGAGAA
AATTTGAATGTGGATTAGATTTTGAATGATATTGGATAATTATTGGTAATTTTATGG
CCTGTGAGAAGGGTGTTGTAGTTTATAAAAGACTGTCTTAATTTGCATACTTAAGCA
TTTAGGAATGAAGTGTTAGAGTGTCTTAAAATGTTTCAAATGGTTTAACAAAATGTA
TGTGAGGCGTATGTGGCAAAATGTTACAGAATCTAACTGGTGGACATGGCTGTTCAT
TGTACTGTTTTTTTCTATCTTCTATATGTTTAAAAGTATATAATAAAAATATTTAAT
TTTTTTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

Figure 2B

AATTTTTAAATTTTTTGTAGAGACAGGGTCTCATTATGTTGCCCAGGGTGGTGTCAA
GCTCCAGGTCTCAAGTGATCCCCCTACCTCCGCCTCCCAAAGTTGTGGGATTGTAGG
CATGAGCCACTGCAAGAAAACCTTAACTGCAGCCTAATAATTGTTTTCTTTGGGATA
ACTTTTAAAGTACATTAAAAGACTATCAACTTAATTTCTGATCATATTTTGTTGAAT
AAAATAAGTAAAATGTCTTGTGAACAAAATGCTTTTTAACATCCATATAAAGCTATC
TATATATAGCTATCTATATCTATATAGCTATTTTTTTTAACTTCCTTTTATTTTCCT
TACAG*GGTTTTAGACAAAATCAAAAAGAAGGAAGGTGCTCACATTCCTTAAATTAA
GGA*GTAAGTCTGCCAGCATTATGAAAGTGAATCTTACTTTTGTAAAACTTTATGGT
TTGTGGAAAACAAATGTTTTTGAACAGTTAAAAAGTTCAGATGTTAGAAAGTTGAAA
GGTTAATGTAAAACAATCAATATTAAAGAATTTTGATGCCAAAACTATTAGATAAAA
GGTTAATCTACATCCCTACTAGAATTCTCATACTTAACTGGTTGGTTGTGTGGAAGA
AACATACTTTCACAATAAAGAGCTTTAGGATATGATGCCATTTTATATCACTAGTAG
GCAGACCAGCAGACTTTTTTTTATTGTGATATGGGATAACCTAGGCATACTGCACTG
TACACTCTGACATATGAAGTGCTCTAGTCAAGTTTAACTGGTGTCCACAGAGGACAT
GGTTTAACTGGAATTCGTCAAGCCTCTGGTTCTAATTTCTCATTTGCAG*GAAATGC
TGGCATAGAGCAGCACTAAATGACACCACTAAAGAAACGATCAGACAGATCTGGAAT
GTGAAGCGTTATAGAAGATAACTGGCCTCATTTCTTCAAAATATCAAGTGTTGGGAA
AGAAAAAAGGAAGTGGAATGGGTAACTCTTCTTGATTAAAAGTTATGTAATAACCAA
ATGCAATGTGAAATATTTTACTGGACTCTTTTGAAAAACCATCTGTAAAAGACTGAG
GTGGGGGTGGGAGGCCAGCACGGTGGTGAGGCAGTTGAGAAAATTTGAATGTGGATT
AGATTTTGAATGATATTGGATAATTATTGGTAATTTTATGGCCTGTGAGAAGGGTGT
TGTAGTTTATAAAAGACTGTCTTAATTTGCATACTTAAGCATTTAGGAATGAAGTGT
TAGAGTGTCTTAAAATGTTTCAAATGGTTTAACAAAATGTATGTGAGGCGTATGTGG
CAAAATGTTACAGAATCTAACTGGTGGACATGGCTGTTCATTGTACTGTTTTTTTCT
ATCTTCTATATGTTTAAAAGTATATAATAAAAATATTTAATTT

Figure 3A

1
CGGGGCCCCACGCTGCGCATCCGCGGGTTTGCTATGGCGATGAGCAGCGGCGGCAGT
GGTGGCGGCGTCCCGGAGCAGGAGGATTCCGTGCTGTTCCGGCGCGGCACAGGCCAG
2
*AGCGATGATTCTGACATTTGGGATGATACAGCACTGATAAAAGCATATGATAAAGC
TGTGGCTTCATTTAAGCATGCTCTAAAGAATGGTGACATTTGTGAAACTTCGGGTAA
ACCAAAAACCACACCTAAAAGAAAACCTGCTAAGAAGAATAAAAGCCAAAAGAAGAA
3
TACTGCAGCTTCCTTACAACAG*TGGAAAGTTGGGGACAAATGTTCTGCCATTTGGT
CAGAAGACGGTTGCATTTACCCAGCTACCATTGCTTCAATTGATTTTAAGAGAGAAA
CCTGTGTTGTGGTTTACACTGGATATGGAAATAGAGAGGAGCAAAATCTGTCCGATC
4
TACTTTCCCCAATCTGTGAAGTAGCTAATAATATAGAACAGAATGCTCAAGAG*AAT
GAAAATGAAAGCCAAGTTTCAACAGATGAAAGTGAGAACTCCAGGTCTCCTGGAAAT
AAATCAGATAACATCAAGCCCAAATCTGCTCCATGGAACTCTTTTCTCCCTCCACCA
5
CCCCCCATGCCAGGGCCAAGACTGGGACCAGGAAAG*CCAGGTCTAAAATTCAATGG
CCCACCACCGCCACCGCCACCACCACCACCCCACTTACTATCATGCTGGCTGCCTCC
6
ATTTCCTTCTGGACCACCA*ATAATTCCCCCACCACCTCCCATATGTCCAGATTCTC
TTGATGATGCTGATGCTTTGGGAAGTATGTTAATTTCATGGTACATGAGTGGCTATC
7
ATACTGGCTATTATATG*GGTTTCAGACAAAATCAAAAAGAAGGAAGGTGCTCACAT
8
TCCTTAAATTAAGGA*GAAATGCTGGCATAGAGCAGCACTAAATGACACCACTAAAG
AAACGATCAGACAGATCTGGAATGTGAAGCGTTATAGAAGATAACTGGCCTCATTTC
TTCAAAATATCAAGTGTTGGGAAAGAAAAAAGGAAGTGGAATGGGTAACTCTTCTTG
ATTAAAAGTTATGTAATAACCAAATGCAATGTGAAATATTTTACTGGACTCTTTTGA
AAAACCATCTGTAAAAGACTGGGGTGGGGGTGGGAGGCCAGCACGGTGGTGAGGCAG
TTGAGAAAATTTGAATGTGGATTAGATTTTGAATGATATTGGATAATTATTGGTAAT
TTTATGGCCTGTGAGAAGGGTGTTGTAGTTTATAAAAGACTGTCTTAATTTGCATAC
TTAAGCATTTAGGAATGAAGTGTTAGAGTGTCTTAAAATGTTTCAAATGGTTTAACA
AAATGTATGTGAGGCGTATGTGGCAAAATGTTACAGAATCTAACTGGTGGACATGGC
TGTTCATTGTACTGTTTTTTTCTATCTTCTATATGTTTAAAAGTATATAATAAAAAT
ATTTAATTTTTTTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

Figure 3B

AATTTTTAAATTTTTTGTAGAGACAGGGTCTCATTATGTTGCCCAGGGTGGTGTCAA
GCTCCAGGTCTCAAGTGATCCCCCTACCTCCGCCTCCCAAAGTTGTGGGATTGTAGG
CATGAGCCACTGCAAGAAAACCTTAACTGCAGCCTAATAATTGTTTTCTTTGGGATA
ACTTTTAAAGTACATTAAAAGACTATCAACTTAATTTCTGATCATATTTTGTTGAAT
AAAATAAGTAAAATGTCTTGTGAACAAAATGCTTTTTAACATCCATATAAAGCTATC
TATATATAGCTATCTATGTCTATATAGCTATTTTTTTTAACTTCCTTTTATTTTCCT
TACAG*GGTTTCAGACAAAATCAAAAAGAAGGAAGGTGCTCACATTCCTTAAATTAA
GGA*GTAAGTCTGCCAGCATTATGAAAGTGAATCTTACTTTTGTAAAACTTTATGGT
TTGTGGAAAACAAATGTTTTTGAACAGTTAAAAAGTTCAGATGTTAAAAAGTTGAAA
GGTTAATGTAAAACAATCAATATTAAAGAATTTTGATGCCAAAACTATTAGATAAAA
GGTTAATCTACATCCCTACTAGAATTCTCATACTTAACTGGTTGGTTATGTGGAAGA
AACATACTTTCACAATAAAGAGCTTTAGGATATGATGCCATTTTATATCACTAGTAG
GCAGACCAGCAGACTTTTTTTTATTGTGATATGGGATAACCTAGGCATACTGCACTG
TACACTCTGACATATGAAGTGCTCTAGTCAAGTTTAACTGGTGTCCACAGAGGACAT
GGTTTAACTGGAATTCGTCAAGCCTCTGGTTCTAATTTCTCATTTGCAG*GAAATGC
TGGCATAGAGCAGCACTAAATGACACCACTAAAGAAACGATCAGACAGATCTGGAAT
GTGAAGCGTTATAGAAGATAACTGGCCTCATTTCTTCAAAATATCAAGTGTTGGGAA
AGAAAAAAGGAAGTGGAATGGGTAACTCTTCTTGATTAAAAGTTATGTAATAACCAA
ATGCAATGTGAAATATTTTACTGGACTCTTTTGAAAAACCATCTGTAAAAGACTGGG
GTGGGGGTGGGAGGCCAGCACGGTGGTGAGGCAGTTGAGAAAATTTGAATGTGGATT
AGATTTTGAATGATATTGGATAATTATTGGTAATTTTATGGCCTGTGAGAAGGGTGT
TGTAGTTTATAAAAGACTGTCTTAATTTGCATACTTAAGCATTTAGGAATGAAGTGT
TAGAGTGTCTTAAAATGTTTCAAATGGTTTAACAAAATGTATGTGAGGCGTATGTGG
CAAAATGTTACAGAATCTAACTGGTGGACATGGCTGTTCATTGTACTGTTTTTTTCT
ATCTTCTATATGTTTAAAAGTATATAATAAAAATATTTAATTT

Figure 4

C212

ACCTGANCCCAGANGGTCAAGGCTGCAGTGAGACGAGATTGCNCCACTGCCCTCCAC
CCTGGGTGATAAGAGTGGGACCCTGTNTCAAAACATACACACACACACACACACACA
CACACACACACACACACACACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTC
TCTCTCTCAAAAACACTTGGTCTGTTATTTTTNCGAAATTGTCAGTCATAGTTATCT
GTTAGACCAAAGCTGNGTAAGNACATTTATTACATTGCCTCCTACAACTTCATCAGC
TAATGTATTTGCTATATAGCAATTACATATNGGNATATATTATCTTNAGGGGATGGC
CANGTNATAAAACTGTCACTGAGGAAAGGA

C272

CCTCCCACCTNAGCCTCCCCAGTAGCTAGGACTATAGGCGTGCNCCACCAAGCTCAG
CTATTTTTNNTATTTAGTAGAGACGGGGTTTCGGCANGCTTAGGCCTCGTNTCGAAC
TCCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTA
GATATTTATTCCCCCTCCCCCTTGGAAAAGTAAGTAAGCTCCTACTAGGAATTTAAA
ACCTGCTTGATCTATATAAAGACAAACAAGGAAAGACAAACATGGGGGCAGGAAGGA
AGGCAGATC

AFM157xd10

TCGAGGTAGATTTGTATTATATCCCATGTACACACACACACACACACACACACACAC
ACACACACACAGACTTAATCTGTTTACAGAAATAAAAGGAATAAAATACCGTTTCTA
CTATACACCAAAACTAGCCATCTTGAC

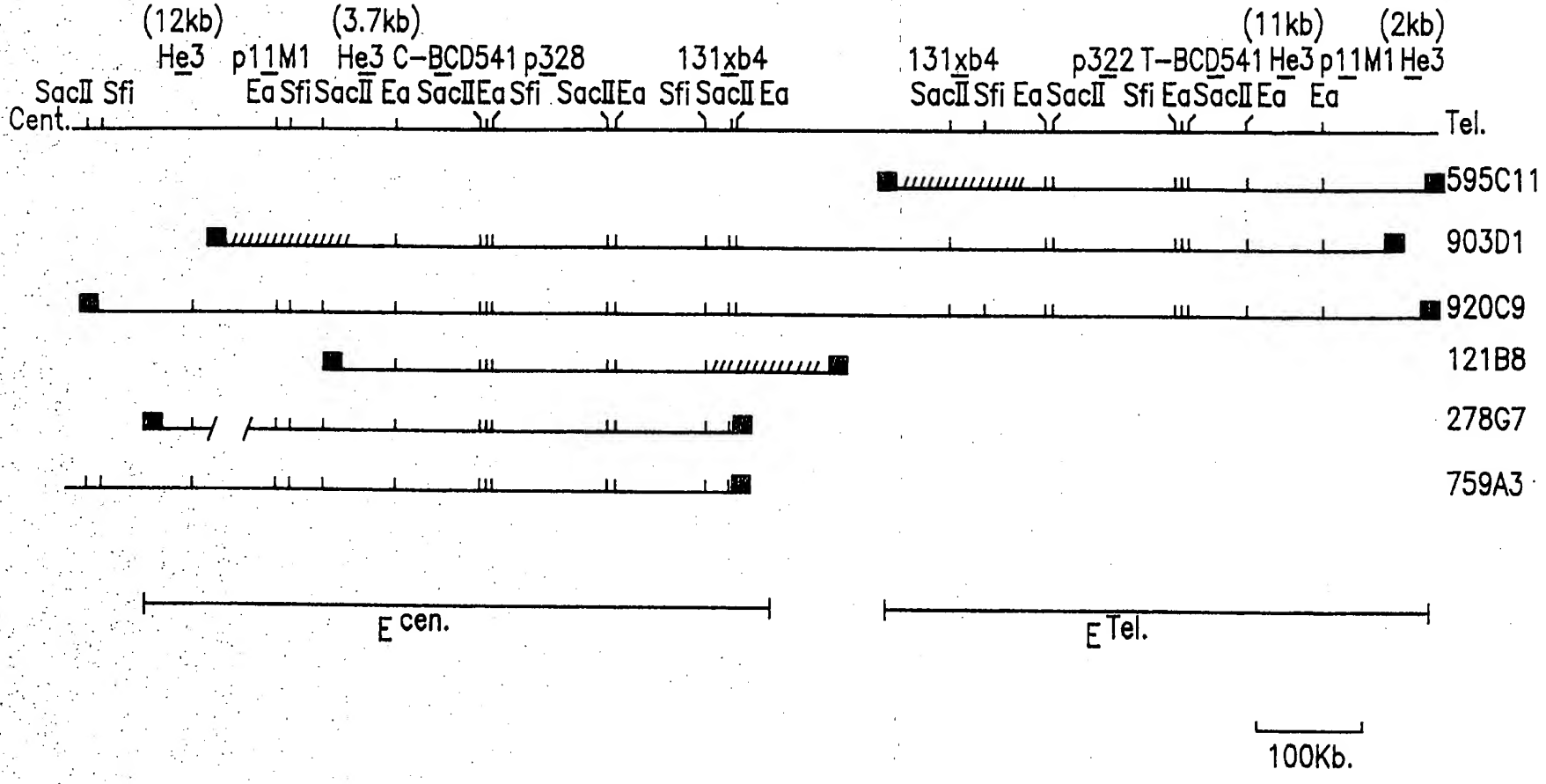
C161

CCCTGAGAAGGCTTCCTCCTGAGTATGCATAAACATTCACAGCTTGCATGCGTGTGT
GTGTGTGTGTGTGTGTGTATGTTTGCTTGCACTGTAAAAACAATTGCAACATCAACA
GAAATAAAAATTAAAGGAATAATTCTCCTCCGACTCTGCCGTTCCATCCAGTGAAAC
TCTTCATTCTGGGGTAAAGTTCCTTCAGTTCTTTCATAGATAGGTATATACTTCATA
AGTCAAACAATCAGGCTGGGTGCAGTAGCTCATGCCTGTAATCCCAGCCCTTTGGGA
GGCCGAGCTGGGCAGATCGA

C171

TCCACCCGCCTTGGCCTCCCAAAGCNCTGGGATTACAGGCGTGACTGCCGCACCCAG
CTGTAAACTGGNTTNNTAATGGTAGATTTTNAGGTATTAACAATAGATAAAAAGATA
CTTTTNGGCATACTGTGTATTGGGATGGGGTTAGAACAGGTGTNCTACCCAAGACAT
TTACTTAAAATCGCCCTCGAAATGCTATGTGAGCTGTGTGTGTGTGTGTGTGTGTGT
GTGTATTAAGGAAAAGCATGAAAGTATTTATGCTTGATTTTTTTTTTTTNACTCATAG
CTTCATAGTGGANCAGATACATAGTCTAAATCAAAATGTTTAAACTTTTTATGTCAC
TTGCTGTC

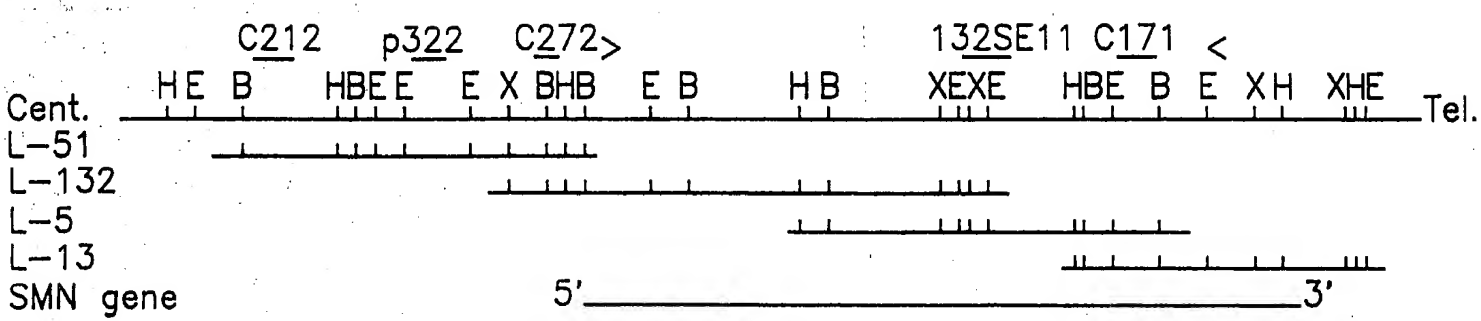
FIG.5



Restriction map of the 5q13 region for EagI(Ea),SacII(SacII),SfiI(Sfi).Numbers under parenthesis indicate the restriction fragment detected by He3; Telomeric element (E_{Tel}),centromeric element (E_{cen}), Centromer(Cent.),Telomere(Tel.).Probes are indicated above the restriction map.YACS are below the restriction map.

REPLACEMENT SHEET

FIG.6



Telomeric element (E^{Tel}) containing the survival motor-neuron gene (SMN gene). Genetic map shows polymorphic markers C212, C272 and C171. Physical map shows location and direction of transcription of SMN gene; phage clones used for assembling physical map. Restriction map for EcoRI(E), XbaI(X), HindIII(H), BglII(B), SacII(S) are shown. Cent. and Tel. indicate centromere and telomere respectively. The position of genomic rearrangements found in SMA patients are also indicated.

GENE DOSAGE ANALYSIS OF THE 5q13 REGION WITH THE 132SE11 PLASMID CONE IN SMA TYPE I PATIENT. TOTAL HUMAN DNA FROM SMA FAMILY WAS DIGESTED WITH HindIII FOR SOUTHERN BLOTTING. FILTER WAS CONSECUTIVELY HYBRIDIZED WITH 132SE11 (A) AND JK53 PROBES (B). A SIGNIFICANT DECREASE IN 132SE11 BAND INTENSITY, WHICH INDICATED THE DELETION, COMPARED WITH THEIR PARENTS. F/FATHER, M/MOTHER, A/AFFECTED

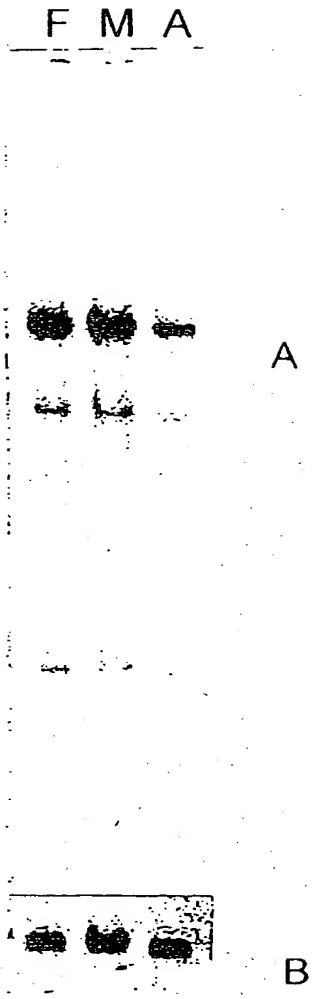


FIG. 7

Figure 8

MAMSSGGSGGGVPEQEDSVLFRRGTGQSDDSDIWDDTALIKAYDKAVASFKHALKNG
DICETSGKPKTTPKRKPAKKNKSQKKNTAASLQQWKVGDKCSAIWSEDGCIYPATIA
SIDFKRETCVVVYTGYGNREEQNLSDLLSPICEVANNIEQNAQENENESQVSTDESE
NSRSPGNKSDNIKPKSAPWNSFLPPPPPMPGPRLGPGKPGLKFNGPPPPPPPPPPHL
LSCWLPPFPSGPPIIPPPPPICPDSLDDADALGSMLISWYMSGYHTGYYM

FIG.9

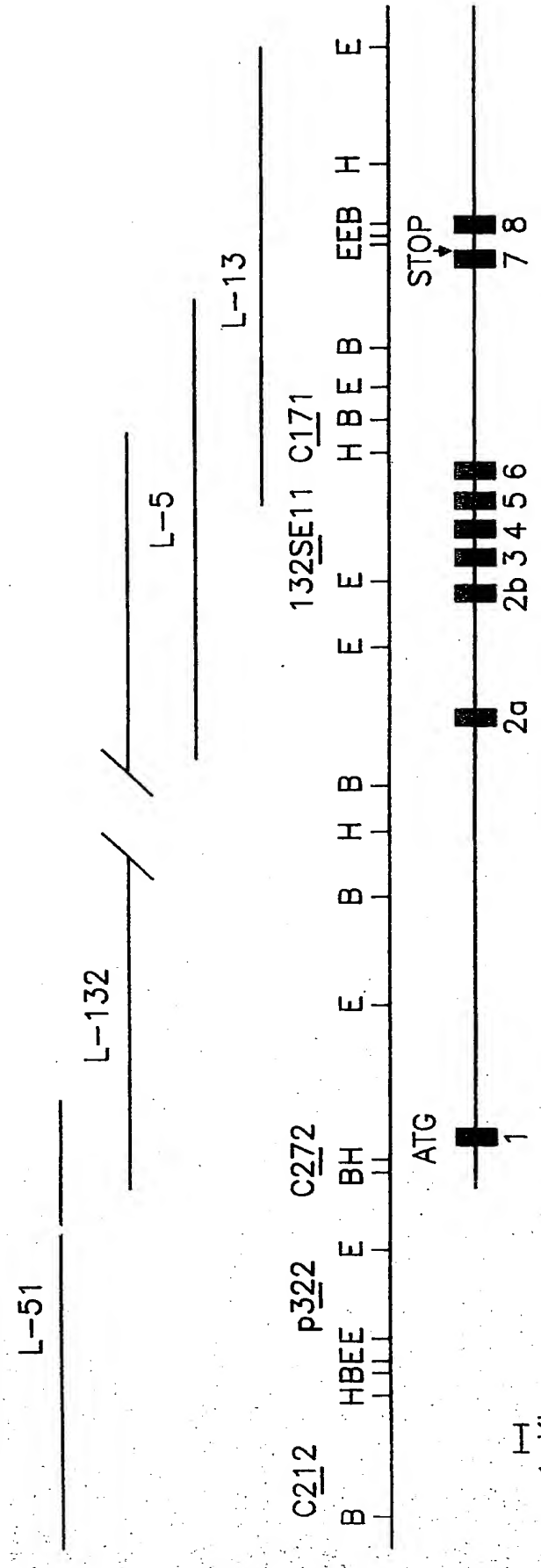


Figure 10A

1

cctcccgggcaccgtactgttccgctcccagaagccccgggcgccggaagtcgtcac
tcttaagaagggacggggccccacgctgcgcacccgcgggtttgct ATG GCG
M A
ATG AGC AGC GGC GGC AGT GGT GGC GGC GTC CCG GAG CAG GAG
M S S G G S G G G V P E Q E
GAT TCC GTG CTG TTC CGG CGC GGC ACA GGC CAG gtgaggtcgcagc
D S V L F R R G T G Q
cagtgcagtctccctattagcgctctcagcacccttcttccggcccaactctccttc
cgca

2a

gtgtaattttgttatgtgtggattaagatgactcttggtactaacatacattttctg
attaaacctatctgnacatgagttgtttttatttcttacccttccag AGC GAT
S D
GAT TCT GAC ATT TGG GAT GAT ACA GCA CTG ATA AAA GCA TAT
D S D I W D D T A L I K A Y
GAT AAA GCT GTG GCT TCA TTT AAG gtatgaaatgcttgnttagtcgttt
D K A V A S F K
tcttattttctcgttattcatttggaaaggaattgataacatacgataaagtgttaa

2b

aggtgctttctgaggtgacggagccttgagactagcttatagtagtaactgggttat
gtcgtgacttttattctgtgcaccaccctgtaacatgtacatttttattcctatttt
cgtag CAT GCT CTA AAG AAT GGT GAC ATT TGT GAA ACT TCG GGT
H A L K N G D I C E T S G
AAA CCA AAA ACC ACA CCT AAA AGA AAA CCT GCT AAG AAG AAT
K P K T T P K R K P A K K N
AAA AGC CAA AAG AAG AAT ACT GCA GCT TCC TTA CAA CAG gttat
K S Q K K N T A A S L Q Q
tttaaaatgttgaggatttaacttcaaaggatgtctcattagtccttatttaatagt
gtaaaatgtctttaact

3

gcctgcaggtcgatcaaaacgagatgatagtttgccctcttcaaaagaaatgtgtgc
atgtatatatctttgatttcttttgtag TGG AAA GTT GGG GAC AAA TGT
W K V G D K C
TCT GCC ATT TGG TCA GAA GAC GGT TGC ATT TAC CCA GCT ACC
S A I W S E D G C I Y P A T
ATT GCT TCA ATT GAT TTT AAG AGA GAA ACC TGT GTT GTG GTT
I A S I D F K R E T C V V V
TAC ACT GGA TAT GGA AAT AGA GAG GAG CAA AAT CTG TCC GAT
Y T G Y G N R E E Q N L S D
CTA CTT TCC CCA ATC TGT GAA GTA GCT AAT AAT ATA GAA CAG
L L S P I C E V A N N I E Q

Figure 10B

```
AAT GCT CAA GAG gtaaggatacaaaaaaaaaaaattcaatttctggaagcag
 N   A   Q   E
agactagatgagaaactgttaaacagtatacaca
4
ccaccgaggcattaatttttcttaatcacacccttataacaaaaacctgcatattt
tttctttttaaag AAT GAA AAT GAA AGC CAA GTT TCA ACA GAT GAA
               N   E   N   E   S   Q   V   S   T   D   E
AGT GAG AAC TCC AGG TCT CCT GGA AAT AAA TCA GAT AAC ATC
 S   E   N   S   R   S   P   G   N   K   S   D   N   I
AAG CCC AAA TCT GCT CCA TGG AAC TCT TTT CTC CCT CCA CCA
 K   P   K   S   A   P   W   N   S   F   L   P   P   P
CCC CCC ATG CCA GGG CCA AGA CTG GGA CCA GGA AAG gtaaacctt
 P   P   M   P   G   P   R   L   G   P   G   K
ctatgaaagttttccagaaaatagttaatgtcgggacatttaacctctctgttaact
aatttgtagctctccca
5
caaatattctgggtaattatttttatccttttggttttgagtccttttttattcctat
catattgaaattggtaagttaattttcctttgaaatattccttatag CCA GGT
                                                  P   G
CTA AAA TTC AAT GGC CCA CCA CCG CCA CCG CCA CCA CCA CCA
 L   K   F   N   G   P   P   P   P   P   P   P   P   P
CCC CAC TTA CTA TCA TGC TGG CTG CCT CCA TTT CCT TCT GGA
 P   H   L   L   S   C   W   L   P   P   F   P   S   G
CCA CCA gtaagtaaaaaagagtataggttagattttgctttcacatacaatttga
 P   P
taatta
6
ccagactttaattttttgtttactggatataaacaatatctttttctgtctccag
ATA ATT CCC CCA CCA CCT CCC ATA TGT CCA GAT TCT CTT GAT
 I   I   P   P   P   P   P   I   C   P   D   S   L   D
GAT GCT GAT GCT TTG GGA AGT ATG TTA ATT TCA TGG TAC ATG
 D   A   D   A   L   G   S   M   L   I   S   W   Y   M
AGT GGC TAT CAT ACT GGC TAT TAT ATG gtaagtaatcactcagcatct
 S   G   Y   H   T   G   Y   Y   M
tttcctgacaatttttttgtagttatgtgactttgtttggtaaatttataaaatact
acttg
7
aactgcagcctaataattgttttctttgggataacttttaaagtacattaaaagact
atcaacttaatttctgatcatattttgttgaataaaataagtaaaatgtcttgtgaa
```

Figure 10C

→ a

acaaaatgcttttaacatccatataaagctatctatatatagctatctatgtctat

→ T

atagctatttttttaacttccttttatttccttacag GGT TTC AGA CAA

G F R Q

AAT CAA AAA GAA GGA AGG TGC TCA CAT TCC TTA AAT taaggagta

N Q K E G R C S H S L N *

aagtctgccagcattatgaaagtgaatcttacttttgtaaaa*ctttatggtttgtgg*

→ g

*aaaaca*aatgttttgaacagttaaaaagttcagatgttaaaaagttgaaaggttaa

tgtaaaacaatcaatattaaagaattttgatgccaaaactattagataaaaggttaa

→ g

tctacatccctactagaattctcatacttaactggttggttatgtggaagaaacata

ctttcacaataaa*gagctttaggatatgatgcc*attttatatcactagtaggcagac

cagcagacttttttttattgtgatatgggataacctaggcatactgcactgtacact

ctgacatatgaagtgctctagtcaagtttaactggtgtccacagaggacatggttta

8

actggaattcgtcaagcctctggttctaatttctcatttgcaggaaatgctggcata

gagcagcactaaatgacaccactaaagaaacgatcagacagatctggaatgtgaagc

gttatagaagataactggcctcatttcttcaaaatatcaagtgttgggaaagaaaaa

aggaagtggaatgggtaactcttcttgattaaaagttatgtaataaccaaatgcaat

→ a

gtgaaatattttactggactcttttgaaaaaccatctagtaaaagactg**g**ggtgggg

gtgggaggccagcacggtggtgaggcagttgagaaaatttgaatgtggattagattt

tgaatgatattggataattattggtaattttatggcctgtgagaagggtgttgtagt

ttataaaagactgtcttaatttgcatacttaagcatttaggaatgaagtgttagagt

gtcttaaaatgtttcaaatggtttaacaaaatgtatgtgaggcgtatgtggcaaaat

gttacagaatctaactggtggacatggctgttcattgtactgtttttttctatcttc

tatatgtttaaaagtatat**aataaa**aatattta

Figure 11

gatctgccttccttcctgccccatgtttgtctttccttgtttgtcttta 50

tatagatcaagcaggttttaaattcctagtaggagcttacatttacttttt 100

ccaaggggggaggggaataaatatcta**cacacacacacacacacacacca** 150
H4TF-1 **GH**

cactggagttcgagacgaggcctaagcaacatgccgaaaccccgtctcta 200
DTF-1

ctaaatacaaaaaatagctgagcttggtggcgcacgcctatagtcctagc 250

tactggggaggctgaggtgggaggatcgcttgagcccaagaagtcgaggc 300
Sp1

tgcagtgagccgagatcgcgccgctgcactccagcctgagcgacagggcg 350

aggctctgtctcaaaacaaacaaacaaaaaaaaaaaaggaaaggaaatata 400
β-IFN

acacagtgaaatgaaaggattgagagaaatgaaaaatatacacgccacaa 450
HiNF-A

atgtgggagggcgataaccactcgtagaaagcgtgagaagttactacaag 500

cggtcctcccgggcaccgtactgttccgctcccagaagccccgggcgccg 550
AP-2

gaagtcgtcactcttaagaagggacggggccccacgctgcgcacccgcgg 600
E4F1

gtttgct ATG GCG ATG AGC AGC GGC GGC AGT GGT GGC 637
M A M S S G G S G G

Figure 12A

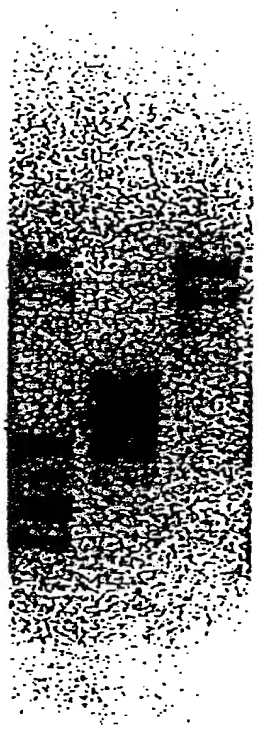
```
cggcgtggtagcaggcc ATG GCG ATG GGC AGT GGC GGA GCG    41
                  Met Ala Met Gly Ser Gly Gly Ala

GGC TCC GAG CAG GAA GAT ACG GTG CTG TTC CGG CGT GGC    80
Gly Ser Glu Gln Glu Asp Thr Val Leu Phe Arg Arg Gly

ACC GGC CAG AGT GAT GAT TCT GAC ATT TGG GAT GAT ACA   119
Thr Gly Gln Ser Asp Asp Ser Asp Ile Trp Asp Asp Thr

GCA TTG ATA AAA GCT TAT GAT AAA GCT GTG GCT TCC TTT   158
Ala Leu Ile Lys Ala Tyr Asp Lys Ala Val Ala Ser Phe

AAG CAT GCT CTA AAG AAC GGT GAC ATT TGT GAA ACT CCA   197
Lys His Ala Leu Lys Asn Gly Asp Ile Cys Glu Thr Pro

GAT AAG CCA AAA GGC ACA GCC AGA AGA AAA CCT GCC AAG   236
Asp Lys Pro Lys Gly Thr Ala Arg Arg Lys Pro Ala Lys

AAG AAT AAA AGC CAA AAG AAG AAT GCC ACA ACT CCC TTG   275
Lys Asn Lys Ser Gln Lys Lys Asn Ala Thr Thr Pro Leu

AAA CAG TGG AAA GTT GGT GAC AAG TGT TCT GCT GTT TGG   314
Lys Gln Trp Lys Val Gly Asp Lys Cys Ser Ala Val Trp

TCA GAA GAC GGC TGC ATT TAC CCA GCT ACT ATT ACG TCC   353
Ser Glu Asp Gly Cys Ile Tyr Pro Ala Thr Ile Thr Ser

ATT GAC TTT AAG AGA GAA ACC TGT GTC GTG GTT TAT ACT   392
Ile Asp Phe Lys Arg Glu Thr Cys Val Val Val Tyr Thr

GGA TAT GGA AAC AGA GAG GAG CAA AAC TTA TCT GAC CTA   431
Gly Tyr Gly Asn Arg Glu Glu Gln Asn Leu Ser Asp Leu

CTT TCC CCG ACC TGT GAA GTA GCT AAT AGT ACA GAA CAG   470
Leu Ser Pro Thr Cys Glu Val Ala Asn Ser Thr Glu Gln

AAC ACT CAG GAG AAT GAA AGT CAA GTT TCC ACA GAC GAC   509
Asn Thr Gln Glu Asn Glu Ser Gln Val Ser Thr Asp Asp

AGT GAA CAC TCC TCC AGA TCG CTC AGA AGT AAA GCA CAC   548
Ser Glu His Ser Ser Arg Ser Leu Arg Ser Lys Ala His
```

Figure 12B

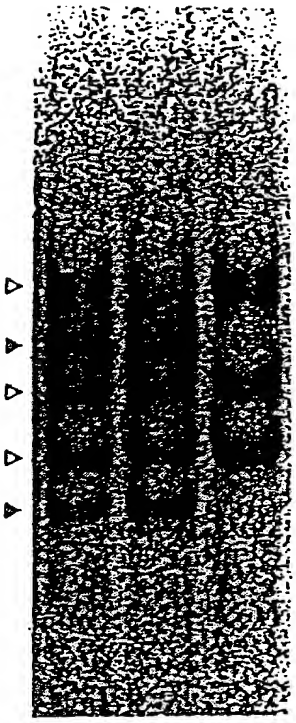
```
AGC AAG TCC AAA GCT GCT CCG TGG ACC TCA TTT CTT CCT   587
Ser Lys Ser Lys Ala Ala Pro Trp Thr Ser Phe Leu Pro

CCA CCA CCC CCA ATG CCA GGG TCA GGA TTA GGA CCA GGA   626
Pro Pro Pro Pro Met Pro Gly Ser Gly Leu Gly Pro Gly

AAG CCA GGT CTA AAA TTC AAC GGC CCG CCG CCG CCG CCT   665
Lys Pro Gly Leu Lys Phe Asn Gly Pro Pro Pro Pro Pro

CCA CTA CCC CCT CCC CCC TTC CTG CCG TGC TGG ATG CCC   704
Pro Leu Pro Pro Pro Pro Phe Leu Pro Cys Trp Met Pro

CCG TTC CCT TCA GGA CCA CCA ATA ATC CCG CCA CCC CCT   743
Pro Phe Pro Ser Gly Pro Pro Ile Ile Pro Pro Pro Pro

CCC ATC TCT CCC GAC TGT CTG GAT GAC ACT GAT GCC CTG   782
Pro Ile Ser Pro Asp Cys Leu Asp Asp Thr Asp Ala Leu

GGC AGT ATG CTA ATC TCT TGG TAC ATG AGT GGC TAC CAC   821
Gly Ser Met Leu Ile Ser Trp Tyr Met Ser Gly Tyr His

ACT GGC TAC TAT ATG GGT TTC AGA CAA AAT AAA AAA GAA   860
Thr Gly Tyr Tyr Met Gly Phe Arg Gln Asn Lys Lys Glu

GGA AAG TGC TCA CAT ACA AAT taag                     885
Gly Lys Cys Ser His Thr Asn  *
```

Figure 13

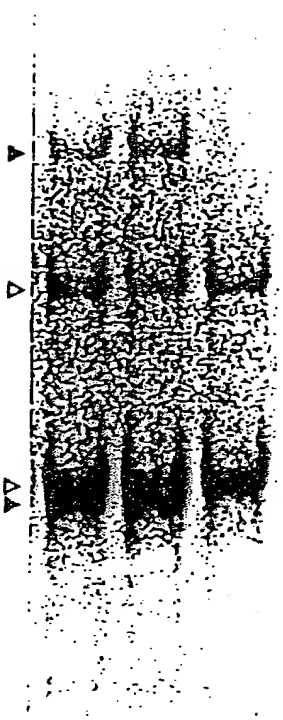
```
 20         30         40         50         60         70
GSGGGVPEQEDSVLFRRGTGQSDDSDIWDDTALIKAYDKAVASFKHALKNGDICETS
====    ====-==========================================
GSGGAGSEQEDTVLFRRGTGQSDDSDIWDDTALIKAYDKAVASFKHALKNGDICETP
          20         30         40         50         60

    80         90        100        110        120        130
GKPKTTPKRKPAKKNKSQKKNTAASLQQWKVGDKCSAIWSEDGCIYPATIASIDFKR
 ===-= -=============--- = ==========-===========-======
DKPKGTARRKPAKKNKSQKKNATTPLKQWKVGDKCSAVWSEDGCIYPATITSIDFKR
  70                  90        100        110        120

      140        150       160        170        180        1
ETCVVVYTGYGNREEQNLSDLLSPICEVANNIEQNAQENENESQVSTDESENSRSPG
========================= =====  ===-=====--=======-== =
ETCVVVYTGYGNREEQNLSDLLSPTCEVANSTEQNTQENE--SQVSTDDSEHSSRSL
    130        140                  160        170        1

90        200        210        220        230        240
NKSDNIKPKSAPWNSFLPPPPPMPGPRLGPGKPGLKFNGPPPPPPPPPPHLLSCWLP
      = =-=== ==========  ================== ===  = ==-=
RSKAHSKSKAAPWTSFLPPPPPMPGSGLGPGKPGLKFNGPPPPPPLPPPPFLPCWMP
80        190        200        210        220        230

  250        260        270        280        290        300
PFPSGPPIIPPPPPICPDSLDDADALGSMLISWYMSGYHTGYYMGFRQNQKEGRCSH
=============== == ===-============================ ===-===
PFPSGPPIIPPPPPISPDCLDDTDALGSMLISWYMSGYHTGYYMGFRQNKKEGKCSH
  240        250        260        270        280        290


SL
-
TN
```



F M A



F M A



F M A

FIG. 14(A) FIG. 14(B) FIG. 14(C)

SSCP ANALYSIS

▼ SMN
▽ C-BCD541

▼▽

121B8 YAC
595CII YAC
HUMAN 1 CONTROL
HUMAN 2 CONTROL
HUMAN 3 CONTROL
HUMAN 4 SMA

FIG. 15